

AMENDMENTS TO THE SPECIFICATION

At page 1, line 4, immediately after the title insert the following new paragraph:

INCORPORATION-BY-REFERENCE OF MATERIAL SUBMITTED
ELECTRONICALLY

Incorporated by reference in its entirety herein is a replacement computer-readable nucleotide/amino acid sequence listing submitted concurrently herewith and identified as follows: One 20,667 Byte ASCII (Text) file named "ReplacementSequenceListing.txt," created on November 4, 2008.

Replace the paragraph beginning at page 6, line 25, and ending at page 6, line 30, with:

In a further preferred embodiment, a passive proton channel according to the invention contains an apoprotein with the consensus sequence L(I)DxxxKxxW(F,Y) (SEQ ID NO: 5). Amino acids given in brackets can in each case replace the preceding amino acid (e.g., LDxxxKxxW (SEQ ID NO: 6), IDxxxKxxW (SEQ ID NO: 7), LDxxxKxxF (SEQ ID NO: 8), LDxxxKxxY (SEQ ID NO: 9), IDxxxKxxF (SEQ ID NO: 10), and IDxxxKxxY (SEQ ID NO: 11)). This consensus sequence is the motif surrounding the retinal-binding amino acid lysine. In bacteriorhodopsin, the "K" at position 6 of the consensus sequence corresponds to K²¹⁶ in the 7th helix of the bacteriorhodopsin.

Replace the paragraph beginning at page 7, line 30, and ending at page 8, line 10, with:

The CHOP-1 protein has a molecular weight of 76 kD and a length of 712 amino acids. It was identified on the basis of overlapping partial cDNA sequences in a *C. reinhardtii* EST database (Asamizu et al., *DNA Research* 7, 305-7 (2000)). Its amino acid sequence is shown in Fig. 1 of the present application. The core protein (amino acids 76-309) includes 7 hypothetical transmembrane segments with 15-20% homology to the sensory archaeal rhodopsins, the ion transporters bacteriorhodopsin (BR) and halorhodopsin (HR), and to an only recently identified rhodopsin from the fungus *Neurospora crassa* (NOP1). Quantitatively, these homology levels are admittedly relatively low, however, on comparison

with BR, those amino acids which define the retinal binding site and the H⁺ transport network in BR are specifically conserved. The consensus motif LDxxxKxxW (SEQ ID NO: 6) observed suggests that in CHOP-1 K²⁹⁶ is the retinal-binding amino acid. 9 out of 22 amino acids which are in direct contact with the retinal in bacteriorhodopsin are identically retained in CHOP-1 and 4 others reflect only conservative changes ((Fig.1); Nagel et al., in preparation).